

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:34:35 ; Search time 23.63 Seconds

(Without alignments)
669.743 Million cell updates/sec

Title: US-09-653-755a-6

Perfect score: 2487

Sequence: 1 EVQLQSGPELVKPGASVWL.....YIAKTTISRSKPGHHHHH 462

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1802	72.5	336	1 GCB_MOUSE	P01866 mus musculu
2	1797	72.3	405	1 GCB_MOUSE	P01867 mus musculu
3	1419	57.1	330	1 GCAA_MOUSE	P01863 mus musculu
4	1414	56.9	399	1 GCAM_MOUSE	P01865 mus musculu
5	1385.5	55.7	335	1 GCAB_MOUSE	P01864 mus musculu
6	1326.5	53.3	333	1 GCB_RAT	P20761 rattus norv
7	1202.5	48.4	329	1 GCC_RAT	P22436 mus musculu
8	1170	47.0	329	1 GC3_MOUSE	P03987 mus musculu
9	1159	46.6	398	1 GC3_MOUSE	P01868 mus musculu
10	1150	46.2	324	1 GCL_MOUSE	P01868 mus musculu
11	1145	46.0	393	1 GCL_MOUSE	P01869 mus musculu
12	1112	44.7	326	1 GCL_RAT	P20759 rattus norv
13	1100	44.2	322	1 GCA_RAT	P0760 rattus norv
14	1087	43.7	330	1 GCL_HUMAN	P01867 homo sapien
15	1080.5	43.4	323	1 GC_RABIT	P01870 oryctolagus
16	1080.5	43.4	329	1 GC2_CAVO	P01862 cavia porce
17	1059	42.6	326	1 GC2_HUMAN	P01859 homo sapien
18	1054.5	42.4	327	1 GC4_HUMAN	P01860 homo sapien
19	776.5	31.2	290	1 GC3_HUMAN	P01860 homo sapien
20	478	19.2	454	1 MUC_HUMAN	P01871 homo sapien
21	477.5	19.2	429	1 EPC_RAT	P01865 rattus norv
22	474	19.1	421	1 EPC_MOUSE	P06336 mus musculu
23	473	19.0	428	1 EPC_HUMAN	P01854 homo sapien
24	462	18.6	118	1 HV51_MOUSE	P06330 mus musculu
25	457.5	18.4	117	1 HV12_MOUSE	P01756 mus musculu
26	457.5	18.4	117	1 HV13_MOUSE	P01757 mus musculu
27	443.5	17.8	438	1 HVC2_HETFR	P23085 heterodontu
28	436.5	17.6	370	1 HVC1_HETFR	P23084 heterodontu
29	431.5	17.4	438	1 HVC5_HETFR	P23087 heterodontu
30	431	17.3	139	1 HV07_MOUSE	P03988 oryctolagus
31	431	17.3	148	1 MUC_RABIT	P01747 mus musculu
32	430.5	17.3	130	1 HV03_MOUSE	P01759 mus musculu
33	429.5	17.3	136	1 HV15_MOUSE	P01759 mus musculu

ALIGNMENTS

RESULT	ID	GC_B_MOUSE	STANDARD	PRT	336 AA.
AC	P01866;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	IG GAMMA-2B CHAIN C REGION.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A. (A ALLELE).				
RX	MEDLINE=80120716; PubMed=6766534;				
RA	Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Odata M., Honjo T.;				
RT	"Complete nucleotide sequence of immunoglobulin gamma2b chain gene				
RT	cloned from newborn mouse DNA.";				
RL	Nature 283:786-789(1980).				
RN	[2]				
RP	SEQUENCE FROM N.A. (MC 11).				
RX	MEDLINE=80081501; PubMed=117548;				
RA	Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;				
RT	"Structure of the constant and 3' untranslated regions of the murine				
RT	gamma 2b heavy chain messenger RNA.";				
RL	Science 206:1299-1303(1979).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=80081502; PubMed=117549;				
RA	Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;				
RT	"Sequence of the cloned gene for the constant region of murine gamma				
RT	2b immunoglobulin heavy chain.";				
RL	Science 206:1303-1306(1979).				
RN	[4]				
RP	SEQUENCE FROM N.A. (B ALLELE).				
RX	MEDLINE=82173203; PubMed=6803173;				
RA	Olio R., Rougeon F.;				
RT	"Mouse immunoglobulin allotypes: post-duplication divergence of gamma				
RT	2a and gamma 2b chain genes.";				
RL	Nature 296:761-763(1982).				
RN	[5]				
RP	CARBOHYDRATE-LINKAGE SITE THR-105.				
RX	MEDLINE=94216359; PubMed=7512967;				
RA	Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.;				
RT	Irimura T., Takahashi N., Kato K., Arata Y.;				
RT	"O-glycosylation in hinge region of mouse immunoglobulin G2b.";				
CC	J. Biol. Chem. 269:12345-12350(1994).				
CC	-1- PPM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAc DISACCHARIDE WHICH IS				
CC	MODIFIED WITH 2 SULFATE ACID RESIDUES.				
CC	-1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOG WITH OTHER IG GAMMA				
CC	CHAINS.				
CC	-1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.				
CC	PIR: A02157; G2MS11.				
DR	InterPro: IPR000495; -				
DR	InterPro: IPR003006; -				
DR	Pfam: PF00047; Ig; 3.				

34	429	17.2	391	1	MUCB_HUMAN	P04220 homo sapien
35	426.5	17.1	393	1	HVC3_HETFR	P23086 heterodontu
36	426.5	17.1	461	1	HVCM_HETFR	P23088 heterodontu
37	421	16.9	479	1	MUCM_RABIT	P04221 oryctolagus
38	420	16.9	450	1	MUC_CANFA	P01874 canis fami
39	417	16.8	457	1	MUC_SUNMU	P20768 sunius fami
40	416.5	16.7	140	1	HV02_MOUSE	P01746 mus musculu
41	416	16.7	137	1	HV11_MOUSE	P01755 mus musculu
42	406.5	16.3	353	1	ALC1_GORGO	P20758 gorilla gor
43	405	16.3	117	1	HV14_MOUSE	P01758 mus musculu
44	401	16.1	120	1	HV50_MOUSE	P06329 mus musculu
45	396.5	15.9	138	1	HV48_MOUSE	P03980 mus musculu

DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 150 210 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 256 314
 FT CARBOHYD 105 105
 FT MOD_RES 336 336
 FT VARIANT 163 163
 FT VARIANT 194 194
 FT VARIANT 300 300
 FT VARIANT 301 301
 FT CONFLICT 25 25
 FT CONFLICT 36 36
 FT CONFLICT 239 239
 SQ SEQUENCE 336 AA; 3658 MW; 7D879662607C356E CRC64;

Query Match 72.5%; Score 1802; DB 1; Length 336;
 Best Local Similarity 100.0%; Pred. No. 2.8e-118;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 AKTTPSVPLAPGCGDTGSSVTLGCLVKGYPRESVTVWNSGLSSSVHTFPALLQSG 178
 DB 1 AKTTPSVPLAPGCGDTGSSVTLGCLVKGYPRESVTVWNSGLSSSVHTFPALLQSG 60
 QY 179 LYTMSSTVPSSTWPSQVTVCSVAHPASSTVDKRLKLEPSGPISTINPCPCCKCHKCPA 238
 DB 61 LYTMSSTVPSSTWPSQVTVCSVAHPASSTVDKRLKLEPSGPISTINPCPCCKCHKCPA 120
 QY 239 PNLGGPSVFIFPPNKKDVLMSLTPKVCVYVDSEDDPDVOISFVNVEVHTAQOT 238
 DB 121 PNLGGPSVFIFPPNKKDVLMSLTPKVCVYVDSEDDPDVOISFVNVEVHTAQOT 180
 QY 299 HREDYSTRVSTPLIOHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 358
 DB 181 HREDYSTRVSTPLIOHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 240
 QY 359 PPPEQLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDPAPVLDSDGSFYISKLN 418
 DB 241 PPPEQLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDPAPVLDSDGSFYISKLN 300
 QY 419 MKTSKEKIDSFSCNVRHGLKNYLLKTTISNPGK 454
 DB 301 MKTSKEKIDSFSCNVRHGLKNYLLKTTISNPGK 336
 RESULT 2
 GCBM_MOUSE
 ID GCBM_MOUSE STANDARD: PRT; 405 AA.
 AC P01867;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-28 CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 335-405 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 RN [2]
 RP SEQUENCE OF 335-378 FROM N.A.

RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 SEGMENT OF MU CHAINS.
 CC -1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
 CHAINS.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE
 IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
 CC -1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
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 or send an email to license@isb.slb.ch).
 CC EMBL: J00462; AAB59659.1; ALT_INIT.
 DR PIR: C02154; GMSBM.
 DR MGI: 96445; Igh-3.
 DR InterPro: IPR000495; -.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Igh_3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
 Alternative splicing.
 FT NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 150 210
 FT DISULFID 256 314
 FT TRANSMEM 352 369
 FT DOMAIN 370 405
 SQ SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49FA CRC64;
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).

Query Match 72.3%; Score 1797; DB 1; Length 405;
 Best Local Similarity 100.0%; Pred. No. 8e-118;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 AKTTPSVPLAPGCGDTGSSVTLGCLVKGYPRESVTVWNSGLSSSVHTFPALLQSG 178
 DB 1 AKTTPSVPLAPGCGDTGSSVTLGCLVKGYPRESVTVWNSGLSSSVHTFPALLQSG 60
 QY 179 LYTMSSTVPSSTWPSQVTVCSVAHPASSTVDKRLKLEPSGPISTINPCPCCKCHKCPA 238
 DB 61 LYTMSSTVPSSTWPSQVTVCSVAHPASSTVDKRLKLEPSGPISTINPCPCCKCHKCPA 120
 QY 239 PNLGGPSVFIFPPNKKDVLMSLTPKVCVYVDSEDDPDVOISFVNVEVHTAQOT 238
 DB 121 PNLGGPSVFIFPPNKKDVLMSLTPKVCVYVDSEDDPDVOISFVNVEVHTAQOT 180
 QY 299 HREDYSTRVSTPLIOHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 358
 DB 181 HREDYSTRVSTPLIOHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 240
 QY 359 PPPEQLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDPAPVLDSDGSFYISKLN 418
 DB 241 PPPEQLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDPAPVLDSDGSFYISKLN 300

QY 419 MKTSKEMKTDSCNVNRHKGKNTYKKTISRSPG 453
 DB 301 MKTSKEMKTDSCNVNRHKGKNTYKKTISRSPG 335

RESULT 3
 GCAM_MOUSE STANDARD; PRT; 330 AA.
 AC P01863;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IG GAMMA-2A CHAIN C REGION, A ALLELE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81076554; PubMed=6777755;
 RA Sikorav J.-L., Auffray C., Rougeon F.;
 RT "Structure of the constant and 3' untranslated regions of the murine
 RT Balb/c gamma 2a heavy chain messenger RNA.";
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81198976; PubMed=6262729;
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 RT and evolution of heavy chain genes: further evidence for intervening
 RT sequence-mediated domain transfer.";
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81223894; PubMed=6787604;
 RA Olio R., Auffray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic
 RT family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RX MEDLINE=74175517; PubMed=4831970;
 RA Bourgois A., Fougereau M., Rocca-Serra J.;
 RT "Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
 RT for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435(1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=73056887; PubMed=4565406;
 RA de Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma 2a
 RT immunoglobulin. Identification of the disulfide bridges.";
 RL Eur. J. Biochem. 30:452-462(1972).

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 CC or send an email to license@isb-sib.ch).

CC EMBL: V00798; CAA24178.1; -
 CC PIR: A02152; G2MSA.
 CC InterPro: IPR000495; -
 CC InterPro: IPR003006; -
 CC Pfam: PF00047; Ig_3.
 CC PROSITE: PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT MOD_RES 330 330
 SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64; REMOVED POST-TRANSLATIONALLY.

Query Match 57.1%; Score 1419; DB 1; Length 330;
 Best Local Similarity 78.6%; Pred. No. 1.1e-91;
 Matches 264; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

QY 119 AKTPPSVYPLAPGCGDTGSSVTLGCLVKGIFPESVVTWNSGSLSSVHTFPALLOG 178
 DB 1 AKTAPSVYPLAPVCGDGTGSSVTLGCLVKGIFPEPYTLTWNSGSLSGVHTFPVLOSD 60
 QY 179 LYTSSSVTPSPSTWPSOTVCSVAHPASSTVYVKLEPSPGISTINPCPCCKECHKCPA 238
 DB 61 LYTSSSVTPSPSTWPSOTVCSVAHPASSTVYVKLEPSPGISTINPCPCCKECHKCPA 114
 QY 239 PNLGGPSVFTFPPIKIDVLMISLTPKVCYVVDSEDDPVOISMFVNNVEVHTAQTOT 298
 DB 115 PNLGGPSVFTFPPIKIDVLMISLTPKVCYVVDSEDDPVOISMFVNNVEVHTAQTOT 174
 QY 299 HREDYNSTIRVSTPLPIODHDMGSKERKCVNNKDLPSLERTISKIKGLVRAPOVYL 358
 DB 175 HREDYNSTIRVSTPLPIODHDMGSKERKCVNNKDLPSLERTISKIKGLVRAPOVYL 234
 QY 359 PPPEAKSRKVSILGLVFNPGDISVEWTSNGTEENYDTPVLDSDSYFYSKLN 418
 DB 235 PPPEAKSRKVSILGLVFNPGDISVEWTSNGTEENYDTPVLDSDSYFYSKLN 294
 QY 419 MKTSKEMKTDSCNVNRHKGKNTYKKTISRSPG 454
 DB 295 VEKKNWVERNSYCSVNHGKLNHTTTSFSRTPK 330

RESULT 4
 GCAM_MOUSE STANDARD; PRT; 399 AA.
 AC P01865;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
 CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
 CC THE A ALLELE.

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CC -----

DR EMBL: J00471: AAB59661.1; ALT_INIT.

DR PIR: A02154: G2MSAM.

DR MGI: MGI:96443: Igh-1.

DR InterPro: IPR000495; -.

DR InterPro: IPR003006; -.

DR Pfam: PF00047: 19; 3.

DR PROSITE: PS00290: IG_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.

KW NON_TER 1

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 144 204

FT DISULFID 250 308

FT TRANSMEM 346 363

FT DOMAIN 364 399

FT CARBOHYD 180 180

FT SEQUENCE 399 AA; 44020 MM; 4C38138FAD3FF0 CRC64; POTENTIAL. CYTOPLASMIC (POTENTIAL). N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 56.9%; Score 1414; DB 1; Length 399; Best Local Similarity 78.5%; Pred. No. 3, 1e-91; Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

OY 119 AKTTPSVYPLABGCGDTGSSVTLGLVKGYPESVYVWNSGLSSSVHTPALLQSG 178
1 AKTTASVYPLAVGCDTGTGSSVTLGLVKGYPPEVTLWNSGLSSSVHTPALLQSD 60

OY 179 LYTMSSVYVPSSTWVSQVYTCVAVHASTYDVKLEPSPSTINPCPKCKCKCPA 238
1 LYTLSSVYVTSSTWVSQVYTCVAVHASTYDVKLEPSPSTINPCPKCKCKCPA 114

OY 239 PNLGGPSVFIPEPNIKDVLMI SLPRKVCVAVDSEDDPVOISFVNVVEVHTAQOT 298
1 PNLGGPSVFIPEPNIKDVLMI SLPRKVCVAVDSEDDPVOISFVNVVEVHTAQOT 174

OY 299 HRDYNSTRVYSTLPIDQDMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 358
1 HRDYNSTRVYSTLPIDQDMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 234

OY 359 PRPAEOLSRKDVSLTGLVGFNPVDISVEMTSGNHTENYKOTAPVLDSDGSVFYISKL 418
1 PRPAEOLSRKDVSLTGLVGFNPVDISVEMTSGNHTENYKOTAPVLDSDGSVFYISKL 294

OY 419 MKTSKWEKTDSEFCNVRHGLKNYLLKTTISRSPG 453
1 MKTSKWEKTDSEFCNVRHGLKNYLLKTTISRSPG 329

DB 295 VEKKNVVERNSYSCSVYHGLNHHHTTKSRTRPG 329

RESULT 5
GCB_MOUSE STANDARD; PRT; 335 AA.
ID GCB_MOUSE P01864;
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2A CHAIN C REGION, B ALLELE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=82037861; PubMed=6170065;
RX Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the

RT IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy chain Cc regions of Ig1a and Ig1b allotypic forms";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -I- MISCELLANEOUS: THE SPOUNCE DIFFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 158 OF THE POSITIONS.
CC -----
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CC -----

DR EMBL: J00479: -; NOT_ANNOTATED_CDS.

DR PIR: A02153: G2MSAB.

DR InterPro: IPR000495; -.

DR InterPro: IPR003006; -.

DR Pfam: PF00047: 19; 3.

DR PROSITE: PS00290: IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1

FT SEQUENCE 335 AA; 36596 MM; FA3382792CBB13C6 CRC64;

Query Match 55.7%; Score 1385.5; DB 1; Length 335; Best Local Similarity 77.1%; Pred. No. 2, 4e-89; Matches 259; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

OY 119 AKTTPSVYPLABGCGDTGSSVTLGLVKGYPESVYVWNSGLSSSVHTPALLQSG 178
1 AKTTASVYPLAVGCDTGTGSSVTLGLVKGYPPEVTLWNSGLSSSVHTPALLQSD 60

OY 179 LYTMSSVYVPSSTWVSQVYTCVAVHASTYDVKLEPSPSTINPCPKCKCKCPA 238
1 LYTLSSVYVTSSTWVSQVYTCVAVHASTYDVKLEPSPSTINPCPKCKCKCPA 119

OY 239 PNLGGPSVFIPEPNIKDVLMI SLPRKVCVAVDSEDDPVOISFVNVVEVHTAQOT 298
1 PNLGGPSVFIPEPNIKDVLMI SLPRKVCVAVDSEDDPVOISFVNVVEVHTAQOT 179

OY 299 HRDYNSTRVYSTLPIDQDMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 358
1 HRDYNSTRVYSTLPIDQDMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 239

OY 359 PRPAEOLSRKDVSLTGLVGFNPVDISVEMTSGNHTENYKOTAPVLDSDGSVFYISKL 418
1 PRPAEOLSRKDVSLTGLVGFNPVDISVEMTSGNHTENYKOTAPVLDSDGSVFYISKL 299

DB 240 PRPAEOLSRKDVSLTGLVGFNPVDISVEMTSGNHTENYKOTAPVLDSDGSVFYISKL 299

OY 419 MKTSKWEKTDSEFCNVRHGLKNYLLKTTISRSPG 454
1 MKTSKWEKTDSEFCNVRHGLKNYLLKTTISRSPG 335

DB 300 VOKSWERGSFLACSVYHGLNHHHTTKSRTRPG 335

RESULT 6
GCB_RAT STANDARD; PRT; 333 AA.
ID GCB_RAT P20761;
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2B CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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RP SEQUENCE FROM N.A.
RA MEDLINE=89232738; Pubmed=3149946;
RL Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR InterPro; IPR000495; -.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; 1g.3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 27 80 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 53.3%; Score 1326.5; DB 1; Length 333;
Best Local Similarity 73.6%; Pred. No. 3e-85;
Matches 248; Conservative 34; Mismatches 50; Indels 5; Gaps 3;

QY 119 AKTTPSVYPLAPCGGDTGSSVTGLGCLVKGYPESTVTVMNSSLSSVHTFPALLQSG 178
DB 1 AQHTAPSVYPLAPCGGDTGSSVTGLGCLVKGYPESTVTVMNSSLSSVHTFPALLQSG 60

QY 179 LYTMSSSVTPSSSTWSPQOTVCSVAHPASSSTVTKLE-PSGPTSTINPCPCCKCHKCP 237
DB 61 LYTLTSSVT--SSWPQOTVCSVAHPASSSTVTKLE-PSGPTSTINPCPCCKCHKCP 116

QY 238 APNLEGGSPVFIFPPNPKDVLMSLTLPKVCVVDVSEDDPQVISMVNNVEHTAQTQ 297
DB 117 VPPELLGSPVFIFPPNPKDVLMSLTLPKVCVVDVSEDDPQVISMVNNVEHTAQTQ 176

QY 298 THREDVNSTIRVSTLPDIOHODMWSGKEPKCKVNNKDLPSPIERTIKIGLVAPQVYI 357
DB 177 PREQDNGSTRVVSALPDIOHODMWSGKEPKCKVNNKDLPSPIERTIKIGLVAPQVYI 236

QY 358 LPPEAOLSRKDVSLTCLVGVGNPDISVEMTSGHTEBNKDTAPVLDSDGSFYISKL 417
DB 237 MGPEPELQDTVSLTCLVGVGNPDISVEMTSGHTEBNKDTAPVLDSDGSFYISKL 296

QY 418 NMKTSKWEKTDSEFCNVRHEGLKNYLLKKTISRSPGK 454
DB 297 NVERSRMDSRAPFCVSVYHGLNHNHHEKISRSPGK 333

RESULT 7
GCC_RAT STANDARD; PRT; 329 AA.
ID AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2C CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=8816903; Pubmed=3127222;
RA Bruggemann M.; Delmastro-Galifre P.; Waldmann H.; Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07189; CAA30169.1; -.
DR PIR; S00847; S00847.
DR InterPro; IPR000495; -.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; 1g.3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B793850773 CRC64;

Query Match 48.4%; Score 1202.5; DB 1; Length 329;
Best Local Similarity 68.2%; Pred. No. 1.2e-76;
Matches 229; Conservative 35; Mismatches 65; Indels 7; Gaps 4;

QY 119 AKTTPSVYPLAPCGGDTGSSVTGLGCLVKGYPESTVTVMNSSLSSVHTFPALLQSG 178
DB 1 AKHTAPSVYPLAPCGGDTGSSVTGLGCLVKGYPESTVTVMNSSLSSVHTFPALLQSG 60

QY 179 LYTMSSSVTPSSSTWSPQOTVCSVAHPASSSTVTKLEPSGPTSTINPCPCCKCHKCPA 238
DB 61 LYTLSSSVTPSSSTWSPQOTVCSVAHPASSSTVTKLEPSGPTSTINPCPCCKCHKCPA 114

QY 239 PNEGGSPVFIFPPNPKDVLMSLTLPKVCVVDVSEDDPQVISMVNNVEHTAQTQ 298
DB 115 DNL-GRPSVFIFPPNPKDVLMSLTLPKVCVVDVSEDDPQVISMVNNVEHTAQTQ 173

QY 299 HREDYNSTIRVSTLPDIOHODMWSGKEPKCKVNNKDLPSPIERTIKIGLVAPQVYI 358
DB 174 HEDQNGSTRVVSALPDIOHODMWSGKEPKCKVNNKDLPSPIERTIKIGLVAPQVYI 233

QY 359 LPPEAOLSRKDVSLTCLVGVGNPDISVEMTSGHTEBNKDTAPVLDSDGSFYISKL 418
DB 234 PPPEAOLSRKDVSLTCLVGVGNPDISVEMTSGHTEBNKDTAPVLDSDGSFYISKL 293

QY 419 MKTSKWEKTDSEFCNVRHEGLKNYLLKKTISRSPGK 454
DB 294 VDTDSWNRGDIYTCVSVYHGLNHNHHTQKNLSRSPGK 329

RESULT 8
GCC_MOUSE STANDARD; PRT; 329 AA.
ID AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85027161; Pubmed=6092053;
RA Wels J.A.; Word C.J.; Rimm D.; Der-Balan G.P.; Martinez H.M.,
```

RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene."
RL EMBL J. 3:2041-2046(1984).
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CC -----
CC EMBL: J00451; NOT_ANNOTATED_CDS.
CC PIR: B02156; G3MSC.
CC InterPro: IPR000495; -
CC InterPro: IPR003006; -
CC Pfam: PF00047; 1g; 3.
CC PROSITE: PS00290; IG_MHC.1.
CC Immunoglobulin C region; Glycoprotein; Transmembrane;
CC Alternative splicing.
CC NON_TER 1 97 CH1.
CC DOMAIN 98 113 HINGE.
CC DOMAIN 114 223 CH2.
CC DOMAIN 224 327 CH3.
CC DOMAIN 329 AA; 36228 MM; F45827174182BAD6 CRC64;
CC SEQUENCE 329 AA; 36228 MM; F45827174182BAD6 CRC64;
Query Match 47.0%; Score 1170; DB 1; Length 329;
Best Local Similarity 66.2%; Pred. No. 2.1e-74;
Matches 221; Conservative 33; Mismatches 74; Indels 6; Gaps 1;
QY 121 TPPSVYPLAPCGDGTGSSVTLGCLVKGYFPEPVTVMTNSGLSSVHTFPALLQSGLY 180
DB 2 TTPSVYPLVPGCSPTGSSSVTLGCLVKGYFPEPVTVKKNYGLSSGVRVSSVLSQGY 61
QY 181 TMSSTVTPSSWPSQTVTCVAHPASSSTVDKLEPSGPISTINPCPPCKECHKCPAPN 240
DB 62 SLSSLYTVSSWPSQTVTCVNAHPASKTELKRIEPR-----IPKSPTPGSSCPNG 115
QY 241 LBGSPVFLFPPIKIVLMISLTPKTYCVVYVSEDDPVQISMFVNNVETHTAQTQTHR 300
DB 116 ILGSPSVFLFPKPKDALMISLTPKTYCVVYVSEDDPVHVSWMFVNKEVHTAMTQPRE 175
QY 301 EDYNSTIRVSTLPLOHODMMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOYILPP 360
DB 176 AOVNSTFRVVALPIOHODMMKGEKCKVNNKALPAPIERTISKKGRAQTPVOYITPP 235
QY 361 PAEOLSRKDVSLTCLVYVGNPDISVEMTNGHTEENYKDTAPVLDSDGSYFIYSKLANK 420
DB 236 PREOMSKKRVSLTCLVYTNFSEALISVEMERNGELEODYKNTPIILSDGYFLYSKLYVD 295
QY 421 TSKWEKTDSCNVHREGIKNYLTKTISRSPK 454
DB 296 TDSWLQGLFETCSVYVHALLNHHHTOKNLSRSPK 329

RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene."
RL EMBL J. 3:2041-2046(1984).
CC -----
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CC -----
CC EMBL: J00451; AAB59655.1; ALT_SEQ.
CC PIR: A02155; G3MSC.
CC InterPro: IPR000495; -
CC InterPro: IPR003006; -
CC Pfam: PF00047; 1g; 3.
CC PROSITE: PS00290; IG_MHC.1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
CC Transmembrane; Alternative splicing.
CC NON_TER 1 97 CH1.
CC DOMAIN 98 113 HINGE.
CC DOMAIN 114 223 CH2.
CC DOMAIN 224 327 CH3.
CC TRANSMEM 346 362 POTENTIAL.
CC DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
CC CONFLICT 342 342 E -> G (IN REF. 2).
CC CONFLICT 388 388 E -> Q (IN REF. 2).
CC SEQUENCE 398 AA; 43929 MM; CF7F264B50A41B95 CRC64;
Query Match 46.6%; Score 1159; DB 1; Length 398;
Best Local Similarity 66.0%; Pred. No. 1.6e-73;
Matches 219; Conservative 33; Mismatches 74; Indels 6; Gaps 1;
QY 121 TPPSVYPLAPCGDGTGSSVTLGCLVKGYFPEPVTVMTNSGLSSVHTFPALLQSGLY 180
DB 2 TTPSVYPLVPGCSPTGSSSVTLGCLVKGYFPEPVTVKKNYGLSSGVRVSSVLSQGY 61
QY 181 TMSSTVTPSSWPSQTVTCVAHPASSSTVDKLEPSGPISTINPCPPCKECHKCPAPN 240
DB 62 SLSSLYTVSSWPSQTVTCVNAHPASKTELKRIEPR-----IPKSPTPGSSCPNG 115
QY 241 LBGSPVFLFPPIKIVLMISLTPKTYCVVYVSEDDPVQISMFVNNVETHTAQTQTHR 300
DB 116 ILGSPSVFLFPKPKDALMISLTPKTYCVVYVSEDDPVHVSWMFVNKEVHTAMTQPRE 175
QY 301 EDYNSTIRVSTLPLOHODMMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOYILPP 360
DB 176 AOVNSTFRVVALPIOHODMMKGEKCKVNNKALPAPIERTISKKGRAQTPVOYITPP 235
QY 361 PAEOLSRKDVSLTCLVYVGNPDISVEMTNGHTEENYKDTAPVLDSDGSYFIYSKLANK 420
DB 236 PREOMSKKRVSLTCLVYTNFSEALISVEMERNGELEODYKNTPIILSDGYFLYSKLYVD 295
QY 421 TSKWEKTDSCNVHREGIKNYLTKTISRSP 452
DB 296 TDSWLQGLFETCSVYVHALLNHHHTOKNLSRSP 327

RESULT 9
GC3M_MOUSE
ID GC3M_MOUSE STANDARD; PRT: 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RX MEDLINE=85027161; Pubmed=6092053;
RA Weis J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

RESULT 10
GC1_MOUSE

ID GC1_MOUSE STANDARD; PRT; 324 AA.
 AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Honjo T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 RT gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=80202559; PubMed=6769752;
 RA Ohta M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
 RT cloned in a bacterial plasmid.";
 RL Gene 9:87-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=80012837; PubMed=113776;
 RA Rogers J., Clarke P., Salsler W.;
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
 RT heavy chain.";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=78242288; PubMed=98524;
 RA Aetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 RT murine myeloma gamma1 chain.";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Swasti J., Milstein C.;
 RT "The disulfide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
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 CC EMBL: V00793; CAA24172.1; -
 CC EMBL: V00793; CAA24173.1; -
 CC EMBL: V00793; CAA24174.1; -
 CC EMBL: V00793; CAA24175.1; -
 CC EMBL: V00795; CAA24176.1; -
 CC PIR: A02159; GIMS
 CC GlycosultedB; P01868; -
 CC MGD: MG1:96446; 19n-4.
 CC InterPro: IPR000495; -
 CC InterPro: IPR003006; -
 CC Pfam: PF00047; 19; 3.
 CC PROSITE: PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 CC Alternative splicing.
 KW NON_TER 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.

FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT DISULFID 244 302
 FT MOD_RES 324 324
 FT CONFLICT 276 276 REMOVED POST-TRANSLATIONALLY.
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812E3D1F2C93 CRC64;
 Query Match 46.28; Score 1150; DB 1; Length 324;
 Best Local Similarity 64.6%; Pred. No. 5.2e-73;
 Matches 217; Conservative 45; Mismatches 62; Indels 12; Gaps 4;
 QY 119 AKTPPSVYPLAPCGDTGSSVTLGCLVKGYPFESVYVYNNSSLSSTVTFPALQSG 178
 DB 1 AKTPPSVYPLAPGSAATNSMTLGLVKGYPFVYVYNNSSLSSTVTFPALQSD 60
 QY 179 LYTSSSVYVPSSTWPSOTVTCVAHPASSSTVTKLEPSSGPISTINPCPCCKCHKCPA 238
 DB 61 LYTSSSVYVPSSTWPSOTVTCVAHPASSSTVTKLEPSSGPISTINPCPCCKCHKCPA 238
 QY 239 PNEGSPVFIFFPNIDVLMISLTPKVCVVDVSDPDVQISWFVNNVHTAQTQT 298
 DB 112 PEVS---SVFIFFPKPKDVLITLTPKVCVVDVSDPDVQISWFVNNVHTAQTQT 168
 QY 299 HREDYNSTIRVSTLPIQHDMMGSKKCKVNNKDLPSPIERTISKIKGLVAPQVYIL 358
 DB 169 REQFNSTFRSVSELPIMHODMLNGKCKRVSNAEPAPLEKTIKTKGRKAPQVYTI 228
 QY 359 PPPEQLSRKVSLTCLVYGFNPDIISVETWSNCHTEENYDTPAVLSDSXYFYSKLN 418
 DB 229 PPPEQNAKDKVSLTCLMTTFEPEDIVYEWQNGQPAENYKNTPTIMNTNGSYFYSKLN 288
 QY 419 MKTSKWEKTDVSCNVRHEGLKNTYLLKRTISRSPPGK 454
 DB 289 VQKSNWEAGNFTQCSVLHGLHNHTKESLSHSPGK 324
 RESULT 11
 GC1_MOUSE STANDARD; PRT; 393 AA.
 ID GC1_MOUSE
 AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Honjo T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 RT gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly
 RT conserved transmembrane sequence and a 28-residue intracellular
 RT domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 RN [3]

RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 RT immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 RN
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
 CC -----
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 CC -----
 CC
 DR EMBL: V00793; CAA24172.1;
 DR EMBL: V00793; CAA24173.1;
 DR EMBL: V00793; CAA24174.1;
 DR PIR: B02159; G1MSN.
 DR MGI: 96446; Igh-4.
 DR InterPro: IPR000495;
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 HINGE.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198 INTERCHAIN (WITH A HEAVY CHAIN).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT DISULFID 244 302
 FT TRANSMEM 340 357
 FT DOMAIN 358 393 POTENTIAL.
 FT SEQUENCE 393 AA; 43386 MW; 4CC8343B7A1CE27 CRC64;
 SO
 Query Match 46.0%; Score 1145; DB 1; Length 393;
 Best Local Similarity 64.5%; Pred. No. 1.5e-72;
 Matches 216; Conservative 45; Mismatches 62; Indels 12; Gaps 4;
 QY 119 AKTTPSVPLAPGCGDITGSSVTLGCLVKGYPESVYTNMNSGSLSSVHFPALQSG 178
 DB 1 AKTTPSVPLAPGSAQNSMTVLGCLVKGYPPEVYTNMNSGSLSSGVHFPALQSD 60
 QY 179 LXTMSSSVTPSPSTWPSQVTCVAHPASTVYDKLBPSTINPCPPCKECHKCPA 238
 DB 61 LXTLSSSVTPSPSPSEVTCVNAHPASTVYDKKIYF-----RDC-GCKPC-ICTIV 111
 QY 239 PULEGSPVFIFPPNKKVLMISLPKVCVVDVSEDDPDVQISFVNNVEVHTAQOT 298
 DB 112 PEVS---SVFIFPPKPKVDLITLTPKVCVVDVSKDDPEVQSWFVDVEVHTAQOT 168

QY 299 HREDYNSTRVSTLPIDQDMWMSGKEFKCKYNNKNDLSPRIERTISKIGLVAPOVYL 358
 DB 169 REQFNFSTRVSSELPFIMQDMLNGKEFKCRVNSAFAPIETIKTGRPARPOVYI 228
 QY 359 PPPAEQLSKRDVSLTCLVGVGPNPDISVEMTSNGHTEENYKDTAPVDSGSEFYISKIN 418
 DB 229 PPKPEQMAKDQVSLTCMINDPEPDIETVEQWNGQPAENYKNTQPIYNTNGSYFYVSKIN 288
 QY 419 MKTSKEKTDSPSCNVRHGLKNYILKTIISRSPG 453
 DB 289 VQKSNMEAGNTFTCSVLHGLHNTKSLSHSPG 323
 RESULT 12
 ID GCL_RAT STANDARD; PRT; 326 AA.
 AC P20759;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8932738; PubMed=3149946;
 RA Bueggenmann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR: PS0017; PS0017.
 DR InterPro: IPR000495;
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 HINGE.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 326 AA; 35946 MW; 013BAB45E4989DA CRC64;
 SO
 Query Match 44.7%; Score 1112; DB 1; Length 326;
 Best Local Similarity 61.9%; Pred. No. 2.3e-70;
 Matches 208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;
 QY 119 AKTTPSVPLAPGCGDITGSSVTLGCLVKGYPESVYTNMNSGSLSSVHFPALQSG 178
 DB 1 AKTTPSVPLAPGALKNSMTVLGCLVKGYPPEVYTNMNSGALSSGVHFPALQSG 60
 QY 179 LXTMSSSVTPSPSTWPSQVTCVAHPASTVYDKLBPSTINPCPPCKECHKCPA 238
 DB 61 LXTLSSSVTPSPSTWPSQVTCVNAHPASTVYDKKIYF-----NCGGDKPC-ICTIG 113
 QY 239 PULEGSPVFIFPPNKKVLMISLPKVCVVDVSEDDPDVQISFVNNVEVHTAQOT 298
 DB 114 SEVS---SVFIFPPKPKVDLITLTPKVCVVDVSDQDEVHFSFVDVEVHTAQTRP 170
 QY 299 HREDYNSTRVSTLPIDQDMWMSGKEFKCKYNNKNDLSPRIERTISKIGLVAPOVYL 358
 DB 171 PEOFNSTRVSSELPILHODMLNGRTFRCKVYSAFSPRIETISKIPGROVPHVYTM 230

RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nle), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE-81208100; PubMed-7236608;
 RA Deisenhofer J.:
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from *Staphylococcus*
 RT aureus at 2.9- and 2.8-A resolution."
 RL Biochemistry 20:2361-2370(1981).
 CC -I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-R, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35, 116, 198, 269 & 272
 CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198, 267&272.
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 CC -----
 DR EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A02146; GHU.
 DR PDB: 1FC1; 15-JUL-92.
 DR PDB: 1FC2; 15-JUL-92.
 DR MIM: 147100;
 DR InterPro: IPR000495; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 1g; 3.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 98
 FT DOMAIN 99 110 CH1.
 FT DOMAIN 111 223 HINGE.
 FT DOMAIN 224 330 CH2.
 FT DISULFID 27 83 CH3.
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT TURN 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT TURN 198 199

FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA3D CRC64;
 Query Match 43.7%; Score 1087; DB 1; Length 330;
 Best Local Similarity 60.8%; Pred. No. 1.3e-68;
 Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;
 QY 119 AKTTPSYVPLAPGCGDVTGSLVGLKGYFPESEVTWNNSLSSVHTFPAILO-S 177
 DB 1 ASTKGPVFLPPLSKSSTGCGTALCLVKDYFPEVYTSNMGALTSVHTFPVALOSS 60
 QY 178 GLYTMSSVTVPSSTWPSQVTGCSVAHPASSTTVDKLEPSPGISTINPCPKCKHCP 237
 DB 61 GLYSLSSTVTPSSSLGDTYICNVNHRKPSNTRKVDKVPKSCDKT-HRCPP-----CP 113
 QY 238 APNLEGGPSVFPPPIKIVYLMISLTPKVTQYVVDYSEDDPVOISMFPNNVYHTAQIQ 297
 DB 114 APDLGGPSVFLPPLSKSSTGCGTALCLVKDYFPEVYTSNMGALTSVHTFPVALOSS 173
 QY 298 THREDYNSTIRVSTPIOHODMMSGKFEKCYNNKDLPSPIERTSKIGLVRAPQVYI 357
 DB 174 PREQYNSTIRVSVTLVYHODMLNKEKCYKSKALPAPLEKITSKAKGPREFQVYT 233
 QY 358 LPPPAQLSRKDVSLTCLVYGFNPBGDISVETWSNGHTEENYKDTAPVLDSDGSYFLYSKL 417
 DB 234 LPPSRDELTKFKNVSLTCLVYGFNPBGDISVETWSNGHTEENYKDTAPVLDSDGSYFLYSKL 293
 QY 418 NAKTSKMEKTDSPSCNVRHREGIKNTYLLAKTISRSPCK 454
 DB 294 TVDKSRMOQGNVSCSVMHDLNHYTOKSLSLSPCK 330
 RESULT 15
 GC_RABIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA CHAIN C REGION.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84030930; PubMed-6313520;
 RA Bernstein K.E., Alexander C.B., Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 RL F-1 haplotype."
 RL Immunogenetics 18:387-397(1983).
 RN [2]
 SEQUENCE OF 1-128.

RX MEDLINE=76135469; PubMed=1243651;
 RA Pratt D.M., Mole L.E.;
 RT "Sequence studies on the constant region of the Fd sections of rabbit
 immunoglobulin G of different allotype.";
 RL Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma
 heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 immunoglobulin G.";
 RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (in) Killander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 Stockholm (1967).
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 MARKERS AND REF.5 THE E15 MARKER.
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 CC -----
 CC EMBL: M16426; AAA31289.1; -.
 DR PIR: A02161; GHRB.
 DR InterPro: IPR000495; -.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; 19; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KM Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT VARIANT 104 104 T -> M (IN D11 MARKER).
 FT VARIANT 185 185 T -> A (IN E15 MARKER).
 FT CONFLICT 48 48 N -> E (IN REF. 2).
 FT CONFLICT 71 71 V -> VPV (IN REF. 2).
 FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
 FT CONFLICT 173 173 Q -> D (IN REF. 5).
 FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
 FT CONFLICT 201 201 N -> D (IN REF. 5).
 FT CONFLICT 218 218 O -> E (IN REF. 5).
 FT CONFLICT 233 233 E -> Q (IN REF. 5).
 FT CONFLICT 246 246 N -> D (IN REF. 5).
 FT CONFLICT 256 256 E -> G (IN REF. 5).
 FT CONFLICT 260 260 N -> D (IN REF. 5).
 FT CONFLICT 266 266 N -> D (IN REF. 5).
 FT CONFLICT 280 280 Y -> W (IN REF. 5).
 FT CONFLICT 284 284 N -> S (IN REF. 5).
 SQ SEQUENCE 323 AA; 35404 MW; 69EBAA118D579A8B CRC64;

Query Match 43.4%; Score 1080.5; DB 1; Length 323;
 Best Local Similarity 61.4%; Pred. No. 3.4e-68;
 Matches 205; Conservative 48; Mismatches 62; Indels 19; Gaps 4;

QY 124 PSYPLAPGCGDTTSSYTLGLVKGTFPESVYTWNSGSLSSVHFPALIQ-SGLYTM 182
 DB 6 PSYPLAPGCCGDTSPSSVTLGLVKGTFPESVYTWNSGSLSSVHFPALIQ-SGLYTM 182
 QY 183 SSSVTVSSSTWPSQTVTCVSAHPASSSTTVDKLKPSPGISINPCPCKCHK--CPAPN 240

DB 66 SSVSVTVSS--SQPTVCNVAHPATNTRKVDKTAPSS-----TCSKPTCPEPE 109
 QY 241 LEGGPSVFIFPPNPKDVMISLTPKRYTCVVVDVSEDDPDVOISFVNNVEVHTAQTQTHR 300
 DB 110 LLGGPSVFIIPPCKPKDMLISRTPEVTCVVVDVSDPDPEVOFTWYINNEQVTRAPPLRE 169
 QY 301 EDVNSTTRVYSTLPIDHODMWSGKEFKCKVNNKPLSPRIERTISKIGLVRAPOVYILPP 360
 DB 170 QQFNSTIRVSTLPITTHODMLRGKEFKCKVNNKALPAIETKISKARQPLEPKVYTWGP 229
 QY 361 PAEOLSRKDVSLTCLVYGFNPGDISVEWTSNGHTEENYKOTAPYLDSDGSYFIYSKIMK 420
 DB 230 PREELSSRSVSLTCMINGFYPSDISVEWENKNGKADENYKTTTPAYLDSGSIYFLNKLSPV 289
 QY 421 TSKWEKTDVFSQCNVRHHEGLKLYLTKTISRSPGK 454
 DB 290 TSEWQRGDVFTCSVMHEALHNHHTQKISRSPGK 323

Search completed: June 18, 2001, 15:34:35
 Job time: 243 sec

